



SEQUENCE LISTING

<110> Board of Regents of the University of Texas System

<120> Mutations in a Novel Photoreceptor-pineal gene 17P cause leber congenital amaurosis (LCA4)

<130> 96606/16UTL

<140> 09/765,061

<141> 2001-01-17

<160> 78

<170> PatentIn version 3.1

<210> 1

<211> 6689

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(6689)

<223> the AIPL1 gene produces aryl-hydrocarbon receptor interacting protein-like 1

<220>

<221> misc\_feature

<222> (1897)..(1906)

<223> n represents any of the four nucleotides A T G or C

<220>

<221> misc\_feature

<222> (3946)..(3946)

<223> n represents any of the four nucleotides A T G or C

<400> 1

ggcctcccaa agtgctggat tacaggcgtg agtcaccgcg cctgggtcccc tgtcttcttt 60  
aagaaagctc agcggacctt tttccttctt ggggtggaac aaaaagccaa atctagcaca 120  
accctgggca gggggcccaga atcactggaa gcaaagggtg atgggatagg aggcgaggct 180  
gcctgtggac cacaggcccc gcccgagtgg ctctgatgag aagccggggc gcctaggtca 240  
ccgccccac cgtctgccct tccccccact cctcctggct gggtaaatcc cagagtctca 300  
gccgcctaag tgtcttcccc ggaggtgaga ttatctccgc ctgtgctgga cacctccctt 360  
tctcctgcag ccatggatgc cgctctgctc ctgaacgtgg aaggggtcaa gaaaaccatt 420  
ctgcacgggg gcacggggcg gtcccaaac ttcacaccg gatcccgagt gaggggggcc 480  
cctccggagc agacagggtc cccacagca gctttcaaca ttccagggtg gcccgaaggc 540  
actgtaaaca gctttcagct gtgccaaaaa aacagccagg cagccccagc gctgggcctc 600  
cggggagctc ccagcgttta ccattcagg gggcattttt ggtactttgc agattcaact 660  
ttagcatggg ctgaggggaa gggcttttgg gaattttctg gggccctaaa tgttgagtga 720  
gaagaaaggg agtccgagga gtcttggtat ttgtcccaa atgtctgtta ggcttcctg 780

gactgaaggg tgcgtctgtg gctacagaat tcgggctttg gccaggcgag gcggtctccg 840  
cctgtaatcc cagcactttg ggaggccaag atgggcagat catgaggtca agagtctcag 900  
accagcctga ccaacatgtg aaaccccatc tctactgaaa atacaaaaat tagccagatg 960  
tgctgtggcg cctgtaatcc cagttcagat actcaggaga cttgaggcag gagaatcact 1020  
tgagcccagg aggtggaggt tgcagtgagc cgagatcata ccactgcact ccaacctggg 1080  
caacagagtg agactctgtc tcagaaaaaa aaaaaaaaaa aagaactcgg gcttacttga 1140  
ggaaggattt ctggacgcac agggctgtgg ggagtggaat ggggtctgta gggaggggtg 1200  
ggtccctcct ccctgggggg tgcaggcagg gtggaggtgc tccaggggtc tgaggcatct 1260  
gatggggtga actgagttag ctgacctggg ggacagccct ggggtgtcggg ggcaaggggg 1320  
tggtctctgc cgggccttga acagtgtgtc tagagcagag tgcaccgtct cgggtgactag 1380  
gtgatctttc atttccgcac catgaaatgt gatgaggagc ggacagtcac tgacgacagt 1440  
cggcaggtgg gccagcccat gcacatcatc atcggaaaca tgttcaagct cgaggtctgg 1500  
gagatcctgc ttacctccat gcgggtgcac gaggtggccg agttctgggt cgacaccatc 1560  
gtaagtaggc cctgcgcgcc tgtctcctgg gactagtctt ttctgggctc acccaccgc 1620  
tttgccgggc tgctgtgttt cgggaaagct gggactcaag cgaagctttg caaagccagt 1680  
cctgcaaact tattccccac cgtgtgcatg tgaagatgga gggaacaagg gctggaaggg 1740  
gtgacccatg ctgtggctgg ctgggtggga gcagggtat gaccagcagg agtgagctgg 1800  
cccacttcac agtcctcaca tctgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 1860  
tgtgtgtgtg agagagagag agagagagag agagagnnnn nnnnnntagc cttaggactt 1920  
attgcagaga ccaacaccta acaatgtaat caggcagcca gtgcaggaca taaataagta 1980  
aggcagtgtg ctttgggcca caaaagcacg ctgagcttgc tggaagccat ggggtccgag 2040  
ctgggggctg ctgagtcagg gccaaagggg gccctccct gcagtaagct ggttctgggg 2100  
cctctccctc ccttgggtcca gctcttaatc ccaacaggct caacagccat ctgcttgtct 2160  
cttcataaaa gaggcagaag gcatttcggg ctaatcccgg ccgggtggggc gggcaggggtg 2220  
acctctgtct ctgtgctggg gacctggagg cagagctgaa ctgctgcata gagtttcagc 2280  
cccttcactt cacatgttgc atgtggggcc agtgctgggt catctcagaa gccgggtcaa 2340  
ggagatgggt tctcaggag cctagttggg gaaactgagg ccagcatac atacagcagg 2400  
cctcgctgag gccgcacggc ggatcttccc agccctcctt catccaagg gtggcaaact 2460  
cagctcccat gctggctgaa gctgtgatga gccagatcta tatctgcacc atctcattta 2520  
atccctacag cagcccta atcgaacagg agcaaccag ggaactgagt ttcagagaag 2580

tgcagagacc tgggctcacc gctaacctgc agcactgcc a ggacaccaa ggcactctct 2640  
tggaccctgg agtcctgctc cttctactgc cccacactgc ccttcctgcg agtcataggc 2700  
tttgagagg tcagggtttc cctggggcag agatgtgtta cagtggacca caagggccag 2760  
aagaggcagc cggaggctaa cagcatatgg cctctggagc caggtttgaa tcctggctgc 2820  
gtcatttctt agctgtgtga ccttaagcaa gttgcttgcg tctctgggct gtagtttccc 2880  
catccgtaaa atgggataat agtgccctgc ttgaattgtc ataaggattg aaggggctca 2940  
taacagtgtg aagtgctttg cctggcacac agttaaccac agttagtatg agtggcatag 3000  
tgagggagca ggattcctcc caggaggggc tctgagtga ggccttttat ggcccaccta 3060  
gctctgggca ggtagcctgg atgccatcca tccgtttatc cccacagcac acgggggtct 3120  
accccatcct rtcccgagc ctgaggcaga tggcccaggg caaggacccc acagagtggc 3180  
acgtgcacac gtgcgggctg gccaacatgt tcgcctacca cacgctgggc tacgaggacc 3240  
tggacgagct gcagaaggag cctcagcctc tggcttttgt gatcgagctg ctgcaggtgg 3300  
ggctgggggtt ggcagggctg gagggctgtg ccagcactgg agagggacag cgggcatcat 3360  
gggcaccccc acccactgg cactggaca gtgcctgtt tctgtttaga taatacgaga 3420  
gggttcataa gccatgggag aatacgaatt tgaaaaaaaa gtcctctgat tttccacaa 3480  
gaaaagtcct ttggtgctgg gcatggtggc ccacgcctgt aatcctagca ctttgggagg 3540  
ccgaggggggt tggatcacct gaggtcagga gttcgaagac cagcctggcc aacatggtaa 3600  
aaccctctct ctattaaaaa caaaaaatt aaccgggtgt ggtggtgcat gcctgtaatc 3660  
aatcccagct acttgggaat ttgaggcagc agaattgctt gaacctggaa gtggaggttg 3720  
cagtgagcag agatcatgtc agtgcatttt aacctgggtg acagagtga actccatgtc 3780  
caaaaaaag aaaaaaaaaa aaagtccact tgggaaccagt ttttaaaat gtgattcatt 3840  
ttcattgtgg aggcatttta tccacttcca ctttcatttt caggagttgg agattataac 3900  
cgctccttg gttcctgtgg tttgtgggtt cagacttggc tctctngtgg cgggagaggc 3960  
tgcattggaac tccccacatc ctcccaacca ggagccccag agtgattggc agcgcggtgt 4020  
tgtggattgg tgagagaggg ttagggccag ggtcaaggc aggtcaggac tcagcttatg 4080  
gccaagactg aggctcagcc tgagagctat gtgggtgaat aaaataaaat aagaactgtg 4140  
tcaaccaagg gcccttaca ggcttgctgt cacagttgtg tggctctgtc actgcacaag 4200  
gtgcaccggc atctctcca aggtgctcat tatagacatt gtatattggc atttccataa 4260  
tgagaagttt ccagcagatg gcaatagtgt attgttctaa caaacgagt attcgtgaca 4320  
atcttctgaa tattagaagt gaagtgtctt gatgaacggg caccttttcc tagtttgcac 4380  
aaagacattg atttagggca gggttttcgg cgttggtgtc tctttccctt gtctgtatgc 4440

acttgaccag	caagcatgac	ttcagggaga	tgtgccacag	ggctctgttt	ttcgggtctc	4500
tgatggggtg	caggccctg	gggtccctgc	ctcactgacc	tgcagctctg	gggccaggtt	4560
gatgccccga	gtgattacca	gagggagacc	tggaacctga	gcaatcatga	gaagatgaag	4620
gcggtgcccc	tcctccacgg	agagggaaat	cggctcttca	agctgggccg	ctacgaggag	4680
gcctcttcca	agtaccagga	ggccatcatc	tgcctaagga	acctgcagac	caaggtcaga	4740
ggccgctggc	caggggtggg	aagtggcgct	gactctgggg	ggcctgcca	gtgccggcca	4800
gggtggggcg	ggggttgggc	agctgcctga	ggcatggct	gaccttctcc	ctgggcagga	4860
gaagccatgg	gaggtgcagt	ggctgaagct	ggagaagatg	atcaatactc	tgatcctcaa	4920
ctactgccag	tgcttctga	agaaggagga	gtactatgag	gtgctggagc	acaccagtga	4980
tattctccgg	caccaccag	gtgcgcgggg	ctgcaggggc	ggacagtgag	ggggcgccca	5040
gcccagggcc	acggagacac	ctgccatagc	cttctctggac	ttttctttcc	accccaccag	5100
ggcaccaaac	cttgtctcca	cccagccggg	tttccccgag	tgtgtaactg	aattgtgggt	5160
gatggatggg	cagtgtctgg	cgcgggcgcg	cctttatattt	aatgtgtgtt	tgaacactta	5220
cccaggaagc	tcgccaagct	tgtgatttca	gcggaacggg	aaacaggcgt	ttaaaaagag	5280
gggcaatcaa	tataggga	aatattatga	tgtcgggtact	agtactgggtg	ttgcgaggat	5340
atggcaccgc	agtactagat	tgacttaatg	ctcgaatcgt	gctcacagta	aaaacatcca	5400
gcccctggct	catgcatcag	gcacacgtcg	tctgcgttta	ttatctcatt	taatcctcat	5460
aatcctcata	atcaccatat	gagggaggtg	cagggaaagg	ggcctgaagg	ttatctaatt	5520
taggtagcgt	ctataagaaa	aataaaacaa	agttatgaat	ataaaattac	tcacagggcc	5580
ttaaaaagga	gaggaggagg	tactgctatt	atgatcatca	tctccatctt	acagttgagg	5640
aaaccgaggg	atgggggata	cagagagggt	aaggatcatg	gcggggctga	gggtcttgga	5700
ggctggtgag	tcccagctgg	gctggggctg	cctctgaggc	tgggaaggga	gctgtagctg	5760
gatgctccct	gctccccaca	ggcatcgtga	aggcctacta	cgtgcgtgcc	cgggctcacg	5820
cagaggtgtg	gaatgaggcc	gaggccaagg	cggacctcca	gaaagtgctg	gagctggagc	5880
cgtccatgca	gaaggcggtg	cgcagggagc	ttgaggctgc	tggagaaccg	catggcgag	5940
aacaggagga	ggagcggtg	cgtgccgga	acatgctgag	ccagggtgcc	acgcagcctc	6000
ccgcagagcc	accacagag	ccaccgcac	agtcatccac	agagccacct	gcagagccac	6060
ccacagcacc	atctgcagag	ctgtccgcag	ggccccctgc	agagccagcc	acagagccac	6120
ccccgtcccc	agggcactcg	ctgcagcact	gagccccctg	aggccacag	ccaccaggc	6180
aggagcaag	tggcctggtc	acttctgggt	cgattgacca	ggatcgtggg	gtcacttttt	6240

```

aaaattttaa  attaatTTTT  gaaatcaaag  tcagacacac  ccatggtaaa  aaaaaaaaaa  6300
aaaacaatcc  caagggTaca  gaagagctta  tgaataaaaag  tagttttctc  ctctaccct  6360
ctcattcctt  ccgtgccatg  gttttaattg  accctgtttt  taattcttct  ggtagttttc  6420
tctatttcca  agtaatctgt  ttaaatcagt  ttctagattt  taccctatgt  caatgacaaa  6480
tgaggatttg  atgctctgat  cttttctcat  gcctgatacc  cctccctgtc  tccccatttt  6540
ggatagttac  atttgggggt  catctcggtg  atttttgtaa  ctttacgcag  gacacttaga  6600
gctctctaga  atccactga  ctttagtggg  gtcttgatgt  agggTgggca  agccccgaca  6660
ctggagctta  gcctgagagg  ggttcttgc  6689

```

```

<210>  2
<211> 1119
<212> DNA
<213> Papio anubis

```

```

<220>
<221> gene
<222> (1)..(1119)
<223> the AIPL1 gene produces aryl-hydrocarbon receptor
interacting protein-like 1

```

```

<400>  2

```

```

atggatgccg  ctctgctcct  gaacgtggaa  ggggtcaaga  aaaccattct  gcacggaggc  60
acgggcgagc  tcccaaactt  catcaccgga  tcccagtgta  tctttcattt  ccgcaccatg  120
aaatgtgatg  aggagcgcac  ggtcatcgac  gacagccggc  aggtggacca  gcccatgcac  180
atcatcatcg  ggaacatggt  caagctcgag  gtctgggaga  tcctgctcac  ctccatgagg  240
gtgcacgagg  tggccgagtt  ctggtgcgac  accatccaca  cgggggtcta  ccccatcctg  300
tcccggagcc  tgcggcagat  ggcccagggc  aaggacccca  cggagtggca  cgtgcacaca  360
tgccggctgg  ccaacatggt  cgctaccac  aactgggct  acgaggacct  ggacgagctg  420
cagaaggagc  ctcagcctct  gatctttgtg  atcgagctgc  tgcaggttga  cgccccgagt  480
gattaccaga  gggagacctg  gaacctgagc  aatcatgaga  agatgaaggt  ggtgcccgtc  540
ctccacggag  agggaaatcg  gctcttcaag  ctgggccgct  acgaggaggc  ctcttccaag  600
taccaggagg  ccatcatctg  cctaaggaac  ctgcagacca  aggagaagcc  atgggaggtg  660
cagtggctga  agctggagaa  gatgatcaac  accctgaccc  tcaactactg  ccagtgcctg  720
ctgaagaagg  aggagtatta  cgaggtgctg  gagcacacca  gtgacattct  ccggcaccac  780
ccaggcatcg  tgaaggccta  ctatgtgcgt  gcccgggctc  acgcagaggt  gtggaatgag  840
gccgaggcca  aggcggacct  ccagaaagtg  ctggagctgg  agccatccat  gcagaaggcg  900

```

gtgcgagg	agctgaggct	gctggagaac	cgcatggcag	agaagcagga	ggaggagcgg	960
ctgcgctgcc	ggaacatgct	gagccaggga	gccacgcagc	ctcccacaga	gccaccggca	1020
gagccccaca	cagcaccacc	tgcgagctg	tccacagggc	cacctgcaga	gccaccgcga	1080
gagctcccc	tgtccccagg	gcactcactg	cagcactga			1119

<210> 3  
 <211> 1155  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> gene  
 <222> (1)..(1155)  
 <223> the AIPL1 gene produces aryl-hydrocarbon receptor  
 interacting protein-like 1

<400> 3		
atggatgccg	ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggggggc 60	
acgggcgagc	tcccaaactt catcaccgga tcccagagtga tctttcattt ccgcaccatg 120	
aaatgtgatg	aggagcggac agtcattgac gacagccggc aggtggggcca gcccatgcac 180	
atcatcatcg	gaaacatggt caagctcgag gtctgggaga tcttgcttac ctccatgcgg 240	
gtgcacgagg	tggccgagtt ctggtgcgac accatccaca caggggtcta ccccatcctg 300	
tcccggagcc	tgaggcagat ggcccagggc aaggaccca cagagtggca cgtgcacaca 360	
tgcgggctgg	ccaacatggt cgctaccac acgctgggct acgaggacct ggacgagctg 420	
cagaaggagc	ctcagcctct ggtctttgtg atcgagctgc tgcaggttga tgccccgagt 480	
gattaccaga	gggagacctg gaacctgagc aatcatgaga agatgaaggc ggtgcccgtc 540	
ctccacggrg	agggaaatcg gctcttcaag ctgggacgct acgaggaggc ctcttccaag 600	
taccaggagg	ccatcatctg cctaaggaac ctgcagacca aggagaagcc gtgggaggtg 660	
cagtggctga	agctggagaa gatgatcaat actctgatcc tcaactactg ccagtgcctg 720	
ctgaagaagg	aggagtacta tgaggtgctg gagcacacca gcgacattct ccggcaccac 780	
ccaggcatcg	tgaaggccta ctacgtgcgt gcccgggctc acgcagaggt gtggaatgag 840	
gccgaggcca	aggcagacct ccggaaagtg ctggagctgg agccgtccat gcagaaggcg 900	
gtgcgagg	agctgaggct gctggagaac cgcatggcgg agaagcagga ggaggagcgg 960	
ctgcgctgcc	ggaacatgct gagccagggt gccacgcagc ctccggcaga gccaccaca 1020	
gagccaccgc	cacagtcatc cacagagcca cctgcagagc caccaccagc accatctgca 1080	
gagctgtccg	cagggccacc tgcagagaca gccacagagc caccaccgtc ccagggcac 1140	
tcgctgcagc	actga	1155

<210> 4  
<211> 1060  
<212> DNA  
<213> Bos taurus

<220>  
<221> gene  
<222> (1)..(1060)  
<223> the AIPL1 gene produces aryl-hydrocarbon receptor  
interacting protein-like 1

<400> 4  
atggatgccca ctctgctcct gaatgtggaa gggatcaaga aaaccattct gcatgggggc 60  
acagggggacc tccccaactt cattactgga gcccgagtga cctttcattt ccgaaccatg 120  
aaatgtgatg aggagcggac ggtgatagac gacagcaagc aggtggggcca tcccatgcac 180  
atcatcattg ggaacatggt caagctggag gtctgggaga tcttgctgac gtccatgcgg 240  
gtcagcgagg tggccgagtt ttggtgcgac accatccaca caggggtcta ccccatcctg 300  
tcccgaggcc tgcggcagat ggcgagggtt aaggaccca cagagtggca cgtgcacacg 360  
tgtggcttgg ccaacatggt cgcttaccac acgctgggct acgaggacct ggacgagctg 420  
cagaaggagc ctcagccact gatcttcata atcgagttgc tgcaggtcga ggccccgagc 480  
cagtaccaga gggagacctg gaacctgaat aaccaggaga agatgcaggc ggtgcccac 540  
ctccatggag aaggaaaccg gctcttcaag ctgggcccgt acgaggaggc ctccaacaag 600  
taccaggaag ccatcgctctg cctgaggaac ctgcagacca aggagaaacc ctgggaggtg 660  
cagtggctga agctggagaa gatgatcaac accctgatcc tgaactactg tcagtgtctg 720  
ctgaagaagg aggagtacta cgaggtgctg gaacacacta gtgacatcct ccggcatcac 780  
ccaggcatcg tgaaggccta ctatgtgagg gcccgggctc acgccgaggt gtggaatgag 840  
gcggaagcca aggcgatct ggagaaagtg ctggagctgg agccgtccat gcggaaggcg 900  
gtgcagaggg agctgaggct gctggagaac cggctggagg agaaacgcga ggaggagcga 960  
ctgcgctgcc ggaacatgct gggctagtgc gcaggcgcca agcctcctgc ctccgcccc 1020  
cgcyctcca cccccccaa aaaaaaaaaa aaaaattttt 1060

<210> 5  
<211> 925  
<212> DNA  
<213> Canis familiaris

<220>  
<221> gene  
<222> (1)..(925)  
<223> the AIPL1 gene produces aryl-hydrocarbon receptor

interacting protein-like 1

```

<400> 5
tgtacggggg caccggcgag ctcccaaact tcctcacggg gtcccgggtc atctttcact    60
tccgcacaac gaaatgcgac gaggcgcgga cagtgatcga cgacagcaag cgtgtggggc    120
atcccatgca catcatcatc gggaacatgt tcaagctgga ggtctgggag gtgctgctga    180
catccatgcg cgtggggcgag gtggccgagt tctgggtgca ctctattcac acaggagtct    240
accccatcct gtcccggagc ctgcggcagg tggcggaggg caaggacccc actgagtggc    300
atgtacacac gtgcggtctg gccaacatgt ttgcctatca cacgctgggc tacgaggacc    360
tggacgagct acagaaggag ccgcagcccc tcatcttcat gatagagctg ctgcaggtgg    420
aggccccaag tgagtaccag agggagacgt ggagcctgaa caatgagaga agatgcagcg    480
gtacccatct catggagagg ggaaccggct cttcaagctg ggccgctaca atgatgcctc    540
caccaagtac caggagccat cgtctgctga ggaacctgca gaccaaggag aagcctggga    600
ggtgcagtgg ctaaagctgg agaagctgat caacaccttg attctcaact actgccagtg    660
tctgctgaag aaggaggagt actacgaggt gctggagcac actagcgaca tcctgcggtc    720
tcaccagga atcgtgaagg cctactacgt gcgcgcccg gctcacgcgg aggtgtggaa    780
cgaggccgag gccagggcgg accttcagaa agtgctggag ctggagccat ccatggggaa    840
ggctgtgcgc agggagctgc ggcttctgga aaatcgctg gaggaaaagc gggaggagga    900
gcggctgcgc tgccggaaca tgcta                                     925

```

```

<210> 6
<211> 1075
<212> DNA
<213> Mus musculus

```

```

<220>
<221> gene
<222> (1)..(1075)
<223> the AIPL1 gene produces aryl-hydrocarbon receptor
interacting protein-like 1

```

```

<400> 6
atggacgtct ctctactcct caatgtggag ggtgtcaaga agaccattct gcatgggggg    60
acaggagagc tccccaactt catcactggc tccagagtga cctttcattt ccgaacaatg    120
aagtgtgatg aagaacgcac ggtgatcgat gacagcaagc aggtggggcca gcccatgagc    180
atcatcatcg gcaacatggt caagctggag gtgtgggaga cgctgctgac ctccatgcgg    240
ctgggcgagg tggttgagtt ctggtgcgac accattcaca caggggtcta ccctatgttg    300
tcccgcagtc tgccggcagg ggctgagggc aaggaccca caagctggca tgtgcacacg    360
tgccgggttg ccaacatggt tgcataccac acgctgggct acgaggacct ggatgagctg    420

```



cagaaagagc	cacagcctct	tgtcttcctg	tatgaactgt	tgcaggtgga	ggccccaat	480
gagtaccaga	gggagacgtg	gaacctgaat	aatgaagaga	ggatgcaggc	ggtacctctt	540
cttcatggag	aaggcaacag	gctctacaag	ctgggacgct	atgatcaggc	cgccaccaag	600
taccaggagg	ccattgtgtg	cctgaggaac	cttcagacca	aggagaagcc	ctgggagggt	660
gagtggctga	agctggagaa	gatgatcaac	accctgatcc	tcaactactg	ccagtgcctg	720
ctgaagaagg	aggagtacta	cgagggtgtg	gagcacacca	gcgacattct	acgacaccac	780
ccagggatcg	tgaaggccta	ctatatgcgc	gcacgtgctc	acgcagaggt	gtggaacgct	840
gaggaggcca	aggcggacct	ggagaaagtg	ctggagttgg	agccatccat	gcgcaaggcg	900
gtgctcaggg	aactgcggt	gctggagagc	cgctggcg	acaaacagga	ggaggagcgg	960
cagcgctgcc	ggagcatgct	gggctaggct	gggctggatt	ccactgagtt	agactgggtt	1020
aggttgggtg	ggagctgcgg	gttgaaccct	ggggcgaggg	ctggggctat	ggact	1075

<210> 7

<211> 1179

<212> DNA

<213> Macaca mulatta

<220>

<221> gene

<222> (1)..(1179)

<223> the AIPL1 gene produces aryl-hydrocarbon receptor interacting protein-like 1

<400> 7

atggatgccg	ctctgctcct	gaacgtggaa	ggggtaaga	aaaccattct	gcacggaggc	60
acgggagagc	tcccaaactt	catcaccgga	tcccagtgga	tctttcattt	ccgcaccatg	120
aaatgtgatg	aggagcgcac	ggatcatcgac	gacagccgtc	aggtggacca	gcccattgcac	180
atcatcatcg	ggaacatgtt	caagctcgag	gtctgggaga	tcttgctcac	ctccatgagg	240
gtgcacgagg	tggccgagtt	ctgggtgcgac	accatccaca	cgggggtcta	ccccatctct	300
tcccggagcc	tgcggcagat	ggcccagggc	aaggacccca	cggagtggca	cgtgcacaca	360
tgcgggctgg	ccaacatgtt	cgcctaccac	acgctgggct	acgaggacct	ggacgagctg	420
cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	cgccccgagt	480
gattaccaga	gggagacctg	gaacctgagc	aatcatgaga	agatgaaggt	ggtgcccgtc	540
ctccacggag	agggaaatcg	gctcttcaag	ytgggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaagcc	gtgggagggt	660
cagtggctga	agctggagaa	gatgatcaac	accctgaccc	tcaactactg	ccagtgcctg	720

ctgaagaagg	aggagtatta	cgaggtgctg	gagcacacca	gtgacattct	ccggcaccac	780
ccaggcatcg	tgaaggccta	ctatgtgctg	gcccgggctc	acgcggaggt	gtggaacgag	840
gccgaggcca	aggcggacct	ccagaaagtg	ctggagctgg	agccatccat	gcagaaggcg	900
gtgcgagggg	agctgaggct	gctggagaac	cgcatggcgg	agaagcagga	ggaggagagg	960
ctgcgctgcc	ggaacatgct	gagccaggga	gccacgcagc	ctcccgcaga	gccaccggca	1020
cagcccccca	cagcaccacc	tgcagagctg	tccacagggc	cacctgcgga	cccaccggcg	1080
gagcccccca	cagcaccacc	tgcggagctg	tccacagggc	cacctgcaga	gccaccgcga	1140
gagctcccc	tgtccccagg	gcactcactg	cagcactga			1179

<210> 8

<211> 1119

<212> DNA

<213> Saimiri sciureus

<220>

<221> gene

<222> (1)..(1119)

<223> the AIPL1 gene produces aryl-hydrocarbon receptor interacting protein-like 1

<400> 8

atggatgccg	ctctgctcct	gaacgtggaa	ggggtaaga	agaccattct	gcacgggggc	60
acgggagagc	tcccaaattt	catcaccgga	tcccagtgga	tctttcattt	ccgcaccatg	120
aaatgtgatg	aggagcggac	ggtgattgac	gacagcaggg	aggtgggcca	gcccattgcac	180
atcatcatcg	ggaacatggt	caagctggag	gtctgggaga	tcctgctcac	gtccatgcgg	240
gtgcgagagg	tggccgagtt	ctggtgcgac	accatccaca	cgggggtcta	ccccatcctg	300
tcccggagcc	tgcggcagat	ggcccagggc	aaggaccgga	cggagtggca	tgtgcacacg	360
tgcgggctgg	ccaacatggt	cgcctaccac	acgctgggct	acgaggacct	ggatgagctg	420
cagaaggagc	ctcagcctct	gatctttgtg	atcgagctgc	tgcaggttga	tgccccaagt	480
gattaccaga	gggagacctg	gaacctgagc	aatcacgaga	agatgaaggt	ggtgcccgtc	540
ctccatggag	aaggaaatag	gctcttcaag	ctgggccgct	acgaggaggc	ctcttccaag	600
taccaggagg	ccatcatctg	cctaaggaac	ctgcagacca	aggagaaacc	ctgggaggtg	660
cagtggctga	agctggagaa	gatgatcaat	accctgatcc	tcaactactg	tcagtgtctg	720
ctgaagaagg	aggagtacta	cgaggtcctg	gagcatacca	gtgacattct	ccggcaccac	780
ccaggcattg	tgaaggccta	ctatgtgcgc	gcccgggctc	acgcggaggt	gtggaacgag	840
gccgaggcca	aggcggacct	ccagaaagtg	ctggagctgg	agccgtccat	gcagaaggcg	900
gtgcgagggg	agctgaggct	gctggagaac	cgcatggcgg	agaagcagga	ggaggagcgg	960

ctgcgctgcc gcaacatgct gagccagggg gccacgtggt ccccgcgga gccacccgca 1020  
gagccacctg cagagtcata cacagagcca cccgcagagc cacctgcaga gccacctgca 1080  
gagctaacct tgaccccgga gcaccacta cagcactga 1119

<210> 9  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(9)  
<223> Amino Acid codon position 79: Met to Thr mutation

<400> 9  
acctccacgc ggggtg 15

<210> 10  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Mutation  
<222> (7)..(9)  
<223> Amino Acid condon 88 mutation: Trp to X

<400> 10  
gagttctgat gcgac 15

<210> 11  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Mutation  
<222> (7)..(9)  
<223> Amino Acid condon Mutation position 96: Val to Ile

<400> 11  
acggggatct acccc 15

<210> 12  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(9)  
<223> Amino Acid codon mutation position 124: Thr to Ile

<400> 12  
gaccccatag agtgg 15

<210> 13  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Mutation  
<222> (7)..(9)  
<223> Amino Acid codon mutation position 376: Pro to Ser

<400> 13  
ccaccctcgt cccca

15

<210> 14  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(9)  
<223> Amino Acid codon mutation position 163: Gln to X

<400> 14  
gattactaga gggag

15

<210> 15  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(9)  
<223> Amino Acid codon mutation position 197: Ala to Pro

<400> 15  
gaggagccct cttcc

15

<210> 16  
<211> 15  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(9)  
<223> Amino Acid codon mutation: TRP 278 X

<400> 16  
gaggtgtgaa atgag

15

<210> 17  
<211> 15  
<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(7)

<223> a to g mutation: IVS2-2A to G

<400> 17

tccccacggc acacg

15

<210> 18

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Glu 262 Ser

<400> 18

cacccaagtg cgcgg

15

<210> 19

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Arg 302 Leu

<400> 19

gcggtgctca gggag

15

<210> 20

<211> 13

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (5)..(5)

<223> deletion of "TGCAGAGCCACC" sequence

<400> 20

gccaccaca gca

13

<210> 21

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Cys 239 Arg

<400> 21

tgccagcgcc tgctg

15

<210> 22

<211> 13

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (5)..(5)

<223> two base deletion: "AG"

<400> 22

tcccgcagcc acc

13

<210> 23

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Cys 42 X

<400> 23

atgaaatgag atgag

15

<210> 24

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(7)

<223> nine base deletion: "CTCCGGCAC"

<400> 24

gatattcacc ca

12

<210> 25

<211> 21

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(7)

<223> eight base insertion: "GTGATCTT"

<400> 25

gactaggtga tcttgtgatc t

21

<210> 26  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(4)  
<223> g to a polymorphism: IVS1-9G to A Benign

<400> 26  
ctcagtgact ag

12

<210> 27  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(4)  
<223> g to c polymorphism: IVS2+66G to C Benign

<400> 27  
tttgccgggc tg

12

<210> 28  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(4)  
<223> c to t polymorphism: IVS2-88C to T Benign

<400> 28  
tcctctcagg ag

12

<210> 29  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(4)  
<223> g to a polymorphism: IVS2-14G to A Benign

<400> 29  
atccatttat cc

12

<210> 30  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(4)  
<223> a to c mutation: IVS2-10A to C Benign

<400> 30  
cgtttctccc ca

12

<210> 31  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(4)  
<223> t to c mutation: IVS3-25T to C Benign

<400> 31  
ctgccccact ga

12

<210> 32  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(7)  
<223> t to c mutation: IVS3-21T to C Benign

<400> 32  
cctcaccgac ct

12

<210> 33  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (7)..(7)  
<223> g to a mutation: IVS5+18G to A Benign

<400> 33  
aggagcggac ag

12

<210> 34  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>



<221> mutation  
<222> (7)..(9)  
<223> Amino Acid codon mutation: Asp 90 His Benign

<400> 34  
tggtgccaca cc

12

<210> 35  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(6)  
<223> Amino Acid mutation: Phe 37 Phe Benign

<400> 35  
catttccgca cc

12

<210> 36  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(6)  
<223> Amino Acid mutation: Ser 78 Ser Benign

<400> 36  
acctctatgc gg

12

<210> 37  
<211> 12  
<212> DNA  
<213> Homo sapiens

<220>  
<221> mutation  
<222> (4)..(6)  
<223> Amino Acid mutation: Cys 89 Cys Benign

<400> 37  
tggtgtgaca cc

12

<210> 38  
<211> 12  
<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: Leu 100 Leu Benign

<400> 38

atcctgtccc gg

12

<210> 39

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: His 172 His

<400> 39

aatcacgaga ag

12

<210> 40

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: Pro 217 Pro Benign

<400> 40

aagccgtggg ag

12

<210> 41

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid codon mutation: Asp 255 Asp Benign

<400> 41

agtgacattc tc

12

<210> 42  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(20)  
<223> 5' to 3' primer sequence

<400> 42  
aagaaaacca ttctgcacgg

20

<210> 43  
<211> 19  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(19)  
<223> 5' to 3' primer sequence

<400> 43  
tgcagctcgt ccaggtcct

19

<210> 44  
<211> 17  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(17)  
<223> 5' to 3' primer sequence

<400> 44  
gacacctccc tttctcc

17

<210> 45  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(18)  
<223> 5' to 3' primer sequence

<400> 45  
gctggggctg cctggctg

18

<210> 46  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(20)  
<223> 5' to 3' primer sequence

<400> 46  
ccgagtgtgatt accagagggga. 20

<210> 47  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(20)  
<223> 5' to 3' primer sequence

<400> 47  
tgagctccag cacctcatag. 20

<210> 48  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(18)  
<223> 5' to 3' primer sequence

<400> 48  
acgcagaggt gtggaatg 18

<210> 49  
<211> 19  
<212> DNA  
<213> Homo sapiens

<220>  
<221> primer\_bind  
<222> (1)..(19)  
<223> 5' to 3' primer sequence

<400> 49  
aaaaagtgac accacgatc

19

<210> 50  
<211> 34  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(34)  
<223> exon/intron - donor splice site:  
CGGATCCCGAgtgagtggggccctccggagca  
ga

<400> 50  
cggatcccga gtgagtgggg ccctccggag caga

34

<210> 51  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Acceptor splice site:  
cagagtgcaccgtctcggtgactagGTGATC  
TTTC

<400> 51  
cagagtgcac cgtctcggtg actaggtgat ctttc

35

<210> 52  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Donor splice site:  
CSACACCATCgtaagtaggcctgcgcgcctgtc  
t

<400> 52  
csacaccatc gtaagtaggc cctgcgcgcc tgtct

35

<210> 53

<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Acceptor splice site:  
gccatccatccgtttatccccacagCACACG  
GGGG

<400> 53  
gccatccatc cgtttatccc cacagcacac ggggg

35

<210> 54  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Donor splice site:  
GCTGCTGCAGgtggggctgggggtggcagggct  
gg

<400> 54  
gctgctgcag gtggggctgg ggttggcagg gctgg

35

<210> 55  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Acceptor splice site:  
cactgacctgcagctctggggccagGTTGA  
TGCCC

<400> 55  
cactgacctg cagctctggg gccaggttga tgccc

35

<210> 56  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)

<223> exon/intron Donor splice site:  
GCAGACCAAGgtcagaggccgctggccacggggt  
g

<400> 56  
gcagaccaag gtcagaggcc gctggccacg ggggtg

35

<210> 57  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Acceptor splice site:  
catggctgaccttctccctgggcagGAGAA  
GCCRT

<400> 57  
catggctgac cttctccctg ggcaggagaa gccrt

35

<210> 58  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Donor splice site:  
CACCACCCAGgtgcgcggggctgcaggggcgga  
ca

<400> 58  
caccacccag gtgcgcgggg ctgcaggggc ggaca

35

<210> 59  
<211> 35  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_binding  
<222> (1)..(35)  
<223> exon/intron Acceptor splice site:  
gctggatgctccctgctccccacagGCATC  
GTGAA

<400> 59  
gctggatgct ccctgctccc cacaggcatc gtgaa

35

<210> 60  
<211> 18  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> exon  
<222> (1)..(18)  
<223> AIPL1 gene exon 1 Primer 5' to 3'

<400> 60  
gga cac ctc cct ttc tcc  
Gly His Leu Pro Phe Ser  
1 5 18

<210> 61  
<211> 18  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> exon  
<222> (1)..(18)  
<223> AIPL1 gene exon 1 Primer 5' to 3'

<400> 61  
gct ggg gct gcc tgg ctg  
Ala Gly Ala Ala Trp Leu  
1 5 18

<210> 62  
<211> 20  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> exon  
<222> (1)..(20)  
<223> AIPL1 gene exon 2 Primer 5' to 3'

<400> 62  
ggg cct tga aca gtg tgt ct  
Gly Pro Thr Val Cys  
1 5 20



<210> 63  
<211> 19  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(19)  
<223> AIPL1 gene exon 2 Primer 5' to 3'

<400> 63  
ttt ccc gaa aca cag cag c  
Phe Pro Glu Thr Gln Gln  
1 5

19

<210> 64  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(18)  
<223> AIPL1 gene exon 3 Primer 5' to 3'

<400> 64  
agt gag gga gca gga ttc  
Ser Glu Gly Ala Gly Phe  
1 5

18

<210> 65  
<211> 20  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(20)  
<223> AIPL1 gene exon 3 Primer 5' to 3'

<400> 65  
tgc cca tga tgc ccg ctg tc  
Cys Pro Cys Pro Leu  
1 5

20

<210> 66  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(18)  
<223> AIPL1 gene exon 4 Primer 5' to 3'

<400> 66  
ttt cgg gtc tct gat ggg  
Phe Arg Val Ser Asp Gly  
1 5

18

<210> 67  
<211> 17  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(17)  
<223> AIPL1 gene exon 4 Primer 5' to 3'

<400> 67  
gca ggc tcc cca gag tc  
Ala Gly Ser Pro Glu  
1 5

17

<210> 68  
<211> 19  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(19)  
<223> AIPL1 gene exon 5 Primer 5' to 3'

<400> 68  
gca gct gcc tca ggt cat g  
Ala Ala Ala Ser Gly His  
1 5

19

<210> 69  
<211> 18  
<212> DNA  
<213> Homo sapiens

<220>  
<221> exon  
<222> (1)..(18)

<223> AIPL1 gene exon 5 Primer 5' to 3'

<400> 69

gtg ggg tgg aaa gaa aag  
Val Gly Trp Lys Glu Lys  
1 5

18

<210> 70

<211> 18

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(18)

<223> AIPL1 gene exon 6 Primer 5' to 3'

<400> 70

ctg gga agg gag ctg tag  
Leu Gly Arg Glu Leu  
1 5

18

<210> 71

<211> 19

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(19)

<223> AIPL1 gene exon 6 Primer 5' to 3'

<400> 71

aaa agt gac acc acg atc c  
Lys Ser Asp Thr Thr Ile  
1 5

19

<210> 72

<211> 384

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(384)

<223> Human AIPL1 Protein

<220>

<221> misc\_feature

<222> (322)..(322)

<223> Xaa represents any of the twenty amino acids

<400> 72

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	
1				5					10					15	
Ile	Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	
				20					25					30	
Ser	Arg	Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	
				35					40					45	
Arg	Thr	Val	Ile	Asp	Asp	Ser	Arg	Gln	Val	Gly	Gln	Pro	Met	His	
				50					55					60	
Ile	Ile	Ile	Gly	Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	
				65					70					75	
Leu	Thr	Ser	Met	Arg	Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	
				80					85					90	
Thr	Ile	His	Thr	Gly	Val	Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	
				95					100					105	
Gln	Met	Ala	Gln	Gly	Lys	Asp	Pro	Thr	Glu	Trp	His	Val	His	Thr	
				110					115					120	
Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	Tyr	His	Thr	Leu	Gly	Tyr	Glu	
				125					130					135	
Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	Gln	Pro	Leu	Val	Phe	Val	
				140					145					150	
Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	Asp	Tyr	Gln	Arg	Glu	
				155					160					165	
Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	Ala	Val	Pro	Val	
				170					175					180	
Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	Arg	Tyr	Glu	
				185					190					195	
Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	Arg	Asn	
				200					205					210	
Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	Leu	
				215					220					225	
Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	
				230					235					240	
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	
				245					250					255	
Ile	Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	
				260					265					270	
Ala	Arg	Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	

275								280				285			
Asp	Leu	Gln	Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala	
				290					295					300	
Val	Arg	Arg	Glu	Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys	
				305					310					315	
Gln	Glu	Glu	Glu	Arg	Leu	Xaa	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly	
				320					325					330	
Ala	Thr	Gln	Pro	Pro	Ala	Glu	Pro	Pro	Thr	Glu	Pro	Pro	Ala	Gln	
				335					340					345	
Ser	Ser	Thr	Glu	Pro	Pro	Ala	Glu	Pro	Pro	Thr	Ala	Pro	Ser	Ala	
				350					355					360	
Glu	Leu	Ser	Ala	Gly	Pro	Pro	Ala	Glu	Pro	Ala	Thr	Glu	Pro	Pro	
				365					370					375	
Pro	Ser	Pro	Gly	His	Ser	Leu	Gln	His							
				380											

<210> 73  
 <211> 384  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> PEPTIDE  
 <222> (1)..(384)  
 <223> Chimpanzee AIPL1 Protein

<400> 73

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	Ile
1				5					10					15	
Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	Ser	Arg
			20					25					30		
Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	Arg	Thr	Val
		35					40					45			
Ile	Asp	Asp	Ser	Arg	Gln	Val	Gly	Gln	Pro	Met	His	Ile	Ile	Ile	Gly
	50					55					60				
Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	Leu	Thr	Ser	Met	Arg
65					70					75					80
Val	His	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	Thr	Ile	His	Thr	Gly	Val
				85					90					95	

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser  
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys  
165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Arg  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala  
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala  
340 345 350

Glu Pro Pro Pro Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala  
355 360 365

Glu Thr Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His  
370 375 380

<210> 74  
<211> 372  
<212> PRT  
<213> Papio anubis

<220>  
<221> PEPTIDE  
<222> (1)..(372)  
<223> Baboon AIPL1 Protein

<400> 74

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser  
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys  
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Thr  
325 330 335

Glu Pro Pro Ala Glu Pro His Thr Ala Pro Pro Ala Glu Leu Ser Thr  
340 345 350

Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu Ser Pro Gly His  
355 360 365

Ser Leu Gln His  
370



<210> 75  
<211> 328  
<212> PRT  
<213> Bos taurus

<220>  
<221> PEPTIDE  
<222> (1)..(328)  
<223> Cow AIPL1 Protein

<400> 75

Met Asp Ala Thr Leu Leu Leu Asn Val Glu Gly Ile Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Asp Leu Pro Asn Phe Ile Thr Gly Ala Arg  
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly His Pro Met His Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
65 70 75 80

Val Ser Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Glu Gly Lys Asp  
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Ile Phe Ile Ile Glu Leu Leu Gln Val Glu Ala Pro Ser  
145 150 155 160

Gln Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Gln Glu Lys Met Gln  
165 170 175

Ala Val Pro Ile Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
180 185 190

Arg Tyr Glu Glu Ala Ser Asn Lys Tyr Gln Glu Ala Ile Val Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Glu  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Gln Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Leu Glu Glu Lys Arg Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Gly  
325

<210> 76  
<211> 328  
<212> PRT  
<213> Mus musculus

<220>  
<221> PEPTIDE  
<222> (1)..(328)  
<223> Mouse AIPL1 Protein

<400> 76

Met Asp Val Ser Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Ser Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg  
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp  
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Val Phe Leu Tyr Glu Leu Leu Gln Val Glu Ala Pro Asn  
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln  
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly  
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg  
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly  
325

<210> 77  
<211> 392  
<212> PRT  
<213> Macaca mulatta

<220>  
<221> PEPTIDE  
<222> (1)..(392)  
<223> Rhesus Monkey AIPL1 Protein

<400> 77

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser  
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys  
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala  
325 330 335

Glu Pro Pro Ala Gln Pro Pro Thr Ala Pro Pro Ala Glu Leu Ser Thr  
340 345 350

Gly Pro Pro Ala Asp Pro Pro Ala Glu Pro Pro Thr Ala Pro Pro Ala  
355 360 365

Glu Leu Ser Thr Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu  
370 375 380

Ser Pro Gly His Ser Leu Gln His  
385 390

<210> 78  
<211> 372  
<212> PRT  
<213> Saimiri sciureus

<220>  
<221> PEPTIDE  
<222> (1)..(372)  
<223> Squirrel Monkey AIPL1 Protein

<400> 78

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile  
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg  
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val  
35 40 45

Ile Asp Asp Ser Arg Glu Val Gly Gln Pro Met His Ile Ile Ile Gly  
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg  
65 70 75 80

Val Arg Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val  
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp  
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala  
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro  
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser  
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys  
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly  
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu  
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys  
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu  
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile  
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg  
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln  
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu  
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg  
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Trp Ser Pro Ala  
325 330 335

Glu Pro Pro Ala Glu Pro Pro Ala Glu Ser Ser Thr Glu Pro Pro Ala  
340 345 350

Glu Pro Pro Ala Glu Pro Pro Ala Glu Leu Thr Leu Thr Pro Gly His  
355 360 365

Pro Leu Gln His  
370

*Bl  
onal*